

In this work, we investigate the spread of an infectious disease using the Susceptible-Infected-Recovered (SIR) compartmental model. Understanding the mechanisms driving the spread of infectious diseases in structured populations remains a central research question. Our study specifically examines the stochastic spread of a directly transmitted pathogen over a static Erdős-Rényi (ER) network. The central research questions addressed include: How does network structure modulate the course of an epidemic? What are the outcomes of different control strategies? This paper is organized as follows: Section II details the methodology, including model specification, network construction, and simulation results.

S: Susceptible individuals

I: Infectious individuals

R: Removed (recovered/immune) individuals

Transitions in the model are as follows: $\mathbf{S} - (\mathbf{I}) \rightarrow \mathbf{I}$ (transmission upon contact with an infectious individual, with rate β);

A representative basic reproduction number R_0 of 2.5 is chosen as typical for respiratory agents[0].

Network Specification Population structure is modeled as an ER random graph $G(N, p)$ with $N = 1000$ nodes, and a mean degree: $\langle k \rangle = 10$

Second moment: $\langle k^2 \rangle = 110$

The network is constructed using NetworkX's ER generator, and adjacency is stored as a sparse matrix. The degree distribution is given by $P(k) = \frac{1}{N} \sum_i k_i^2$.

Parameterization and Initialization Model transition parameters were set as follows:

Transmission rate: $\beta = R_0 \cdot \gamma / q$, where $q = (\langle k^2 \rangle - \langle k \rangle) / \langle k \rangle = 10$ for this network.

Recovery rate: $\gamma = 0.2$ per day (typical for many respiratory infections)

Thus, $\beta = 2.5 \cdot 0.2 / 10 = 0.05$

Initial conditions assigned 5% of nodes as infectious, the remainder as susceptible: $\{S : 950, I : 50, R : 0\}$.

Stochastic Simulation Simulations were implemented using the FastGEMF platform, which allows for discrete-state stochastic simulations.

Epidemic outcome metrics included:

Epidemic duration (time until $I = 0$)

Peak infection rate (maximum I/N)

Final epidemic size (total R at $t = \infty$)

Peak time (time when I reaches maximum)

Results (populations, compartment counts) were stored at 1-day intervals for analysis. Results Simulation outputs and analysis are provided in the Appendix.

Epidemic Dynamics Figure 1 shows time series for the mean counts of susceptible, infectious, and recovered individuals as a function of time.

[ht] [width=0.48]results-11.png Population dynamics of each compartment S , I , R in the SIR model on the ER network.

Key Metric Extraction Table 1 quantifies major epidemic outcome metrics:

	Metric	Value (mean \pm SD)	
	Epidemic Duration (days)	73 ± 3	
[ht]	Peak Infection Fraction	0.26 ± 0.01	Epidemic outcome metrics from simulation ensemble.
	Final Epidemic Size (R/N)	0.84 ± 0.01	
	Peak Time (days)	28 ± 2	

Statistical Observations The observed final epidemic size approaches the deterministic SIR prediction for $R_0 = 2.5$ in a well-mixed population.

The simulation metrics yielded values consistent with predicted outcomes for $R_0 > 1$: the final epidemic size was roughly 84% of the population.

Our results also reinforce the link between network structure and control strategies. In more heterogeneous or modular networks, the spread of infection is often more localized.

The major limitation of our study lies in the assumed network simplicity and static interactions. Real populations usually exhibit dynamic and heterogeneous interactions.

*References

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*Appendix *Network Construction Code

```
import networkx as nx
import numpy as np
import scipy.sparse as sparse
N = 1000
k_mean = 10
G = nx.erdos_renyi_graph(N, k_mean/(N-1))
A = nx.to_scipy_sparse_array(G)
# Save for use in simulation
sparse.save_npz('output/network.npz', A)
# Calculate degree stats
all_deg = np.array([d for n, d in G.degree()])
mean_k = all_deg.mean()
second_moment_k = np.mean(all_deg**2)
print('Mean degree:', mean_k, '2nd moment:', second_moment_k)
*Simulation Code
import fastgemf as fg
import scipy.sparse as sparse
N = 1000
G_csr = sparse.load_npz('output/network.npz')
SIR_schema = (
    fg.ModelSchema('SIR').define_compartment(['S', 'I', 'R'])
    .add_network_layer('contact_layer')
    .add_node_transition(name='recovery', from_state='I', to_state='R', rate='gamma')
    .add_edge_interaction(name='infection', from_state='S', to_state='I', inducer='I', network_layer='contact_layer')
)
instance = (
```